

Claea dafangensis (Cypriniformes, Nemacheilidae), a new cave-dwelling fish from the upper Wujiang River, Guizhou Province, China

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Abstract

A new species of the genus *Claea*, *Claea dafangensis* **sp. nov.**, is described from Yuchong Township, Dafang County, Guizhou Province, China. This species can be distinguished from its four congeners by a combination of the following characteristics: body pigmentation present; normal eyes with a diameter of 10.9–21.0% of head length (HL); processus dentiformis prominent, covering the lower jaw when the mouth is shut; 8–9 branched pectoral-fin rays; 16 branched caudal-fin rays; caudal-peduncle depth 6.1–8.7% of standard length (SL); interorbital width 23.6–39.0% HL; tip of maxillary barbel reaching the posterior margin of the eyes; out-rostral barbel extending backward beyond the anterior nostrils; and anal-fin base length 4.0–5.5% SL. Mitochondrial Cyt *b* analysis further supports the distinctiveness of this population, revealing that it forms an independent phylogenetic lineage with a minimum genetic distance of 2.6% from *C. wulongensis*. The description of this new species suggests that *Claea dabryi* represents a species complex containing multiple distinct lineages, the diversity of which requires further evaluation.

Key Words

Mitochondrial, morphology, taxonomy, Wujiang basin

Introduction

The mountain loach genus *Claea* was established by Kottelat in 2011, with *Oreias dabryi* as the type species (Kottelat 2011). *Oreias dabryi* was previously classified under the genus *Oreias* Sauvage 1874, which had long been recognized as a valid genus in research papers and monographs (Kaup 1829; Temminck and Laugier de Chartrouse 1838; Nichols 1944; Cao and Wu 1962; Bănărescu and Nalbant 1976; Zhu and Cao 1988; Zhu 1989; Chu and Chen 1990; Zhou and Cui 1993), lead-

ing to persistent controversy. However, Kottelat (2011) considered *Oreias* a junior homonym of *Oreias* Kaup, 1829, and *Oreias* Temminck, 1838, as the name had already been used in Aves taxonomy. This proposal gained widespread acceptance, and the genus name *Claea* is now recognized as the valid genus (Kottelat 2012; Zhang et al. 2024; Lei et al. 2025). Recently, Zhang et al. (2024) conducted a systematic revision of the genus *Claea* and confirmed its taxonomic validity. To date, four valid species have been recorded from the Yangtze River and its tributaries: *C. dabryi* (Sauvage 1874), *C. minibarba* Zhang,

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Luo, Huang & Zhang, 2024, *C. scet* Lei, He, Huang, Zhou & He, 2025, and *C. wulongensis* (Chen, Sheraliev, Shu & Peng, 2021) (Zhang et al. 2024; Lei et al. 2025) (Fig. 1).

Claea dabryi, previously recorded as the subspecies *Schistura dabryi dabryi* (Zhu 1989), was once considered a widely distributed species throughout the Yangtze River basin in southern China, including Sichuan (Zhu 1989; Guo et al. 2021), northern Yunnan (Zhu 1989; Tian et al. 2022), western Guizhou (suburbs of Bijie; Zhu 1989), and western Hubei (Zhu 1989; Guo et al. 2021). Recently, populations from southern Chongqing and western Hubei have been described as distinct species, i.e., *C. wulongensis* (Chen, Sheraliev, Shu & Peng, 2021) (formerly assigned to *Triplophysa* Chen et al., 2021) and *C. minibarba* Zhang, Luo, Huang & Zhang, 2024 (Zhang et al. 2024), respectively—suggesting that *C. dabryi* may represent a species complex with underestimated diversity. Although *C. dabryi* has been reported from a tributary of the upper Wujiang River near Bijie City, Guizhou Province (Zhu 1989), the considerable straight-line distance (~500 km) from its type locality in Dengchigou, Baoxing County, Sichuan Province (Kottelat 2012), together with the intervening Wumeng Mountains and hydrological isolation by the Jingshaji River (Fig. 1), casts doubt on the identity of the Guizhou population. Given the low dispersal ability of loach species, geographically isolated populations are prone to divergence and speciation. Thus, the Guizhou population may not represent true *C. dabryi*, and further taxonomic and genetic studies are needed to clarify its taxonomic status.

From 2018 to 2024, we conducted a comprehensive survey of aquatic vertebrate diversity in the upper Yangtze River basin, during which 14 specimens of the genus *Claea* were collected. Detailed morphological examinations and mitochondrial cytochrome *b* (Cyt *b*) phylogenetic analyses revealed genetic divergence between these specimens and all currently recognized species in the genus. Based on morphological distinctiveness and molecular evidence, we formally describe the population from Dafang County, Guizhou Province, China, as a new species herein.

Materials and methods

Sampling and morphological data collection

During field surveys conducted between 2018 and 2024, we collected a total of 17 specimens, including 14 specimens of the new species from the Yuchong River, a tributary of the Wujiang River in Dafang County, Guizhou Province, and three specimens of *C. dabryi* from Wenchuan County, Sichuan Province, China. All specimens were initially fixed in 10% buffered formalin and transferred to 75% ethanol for preservation, with muscle tissues for molecular analysis preserved in 95% alcohol at -20°C. All materials are deposited at Guizhou Normal University (GZNU), Guiyang, Guizhou Province, China.

For morphological comparisons, we contacted the authors of *C. minibarba* and *C. wulongensis* and obtained their morphological data with their assistance, which we incorporated into our statistical analyses.

DNA extraction, PCR, and sequencing

We sequenced three samples from the genus *Claea*. Genomic DNA was extracted from muscle tissues using a DNA extraction kit (Tiangen Biotech Co., Ltd., Beijing, China). The primers used for Cyt *b* were L14737 (5'-CCACCGTTGT-TAATTCAACTAC-3') and H15915 (5'-CTCCGATCTC-CGGATTACAAGAC-3'), following Xiao et al. (2005). PCR amplifications were performed in a 25 µL reaction volume with the following cycling conditions: an initial denaturing step at 95°C for 3 min; 35 cycles of denaturing at 94°C for 50 s, annealing at 52°C for 1 min, extension at 72°C for 1 min, and a final extension step at 72°C for 10 min. The PCR products were sequenced on an ABI Prism 3730 automated DNA sequencer at Chengdu TSING KE Biological Technology Co., Ltd. (Chengdu, China) (Table 1).

Morphometrics, comparisons, and statistics

Morphometric data were collected from 17 well-preserved specimens of the genus *Claea* (Suppl. material 1). Twenty measurements were recorded to the nearest 0.1 mm with digital calipers following the protocols of Tang et al. (2012). All measurements were taken on the left side. Principal component analyses (PCAs) of size-corrected measurements and simple bivariate scatterplots were used to characterize the morphometric differences between the new species and closely related species. Multivariate analysis of variance was used to determine the significance of differences in morphometric characteristics between the new species and similar species. All statistical analyses were performed using SPSS 21.0 (SPSS, Inc., Chicago, IL, USA), and differences were considered statistically significant at $P < 0.05$. In addition, as reported by other researchers (Parsons and Jones 2000; Polaszek et al. 2004), canonical discriminant analysis (CDA, George and Mallery 2010) was used to classify individuals into different groups, where a priori membership was determined based on specimens belonging to different species.

Phylogenetic analyses and genetic distance

Forty-seven mitochondrial Cyt *b* sequences, including three newly sequenced and 44 downloaded from GenBank, were used for molecular analysis. We followed the phylogenetic study of Luo et al. (2023) and used *Barbatula labia*, *B. barbatula*, and *Homatula berezowskii* as outgroups (Table 1).

All sequences were assembled and aligned using the MUSCLE (Edgar 2004) module in MEGA v. 7.0 (Kumar et al. 2016) with default settings. Alignment results were

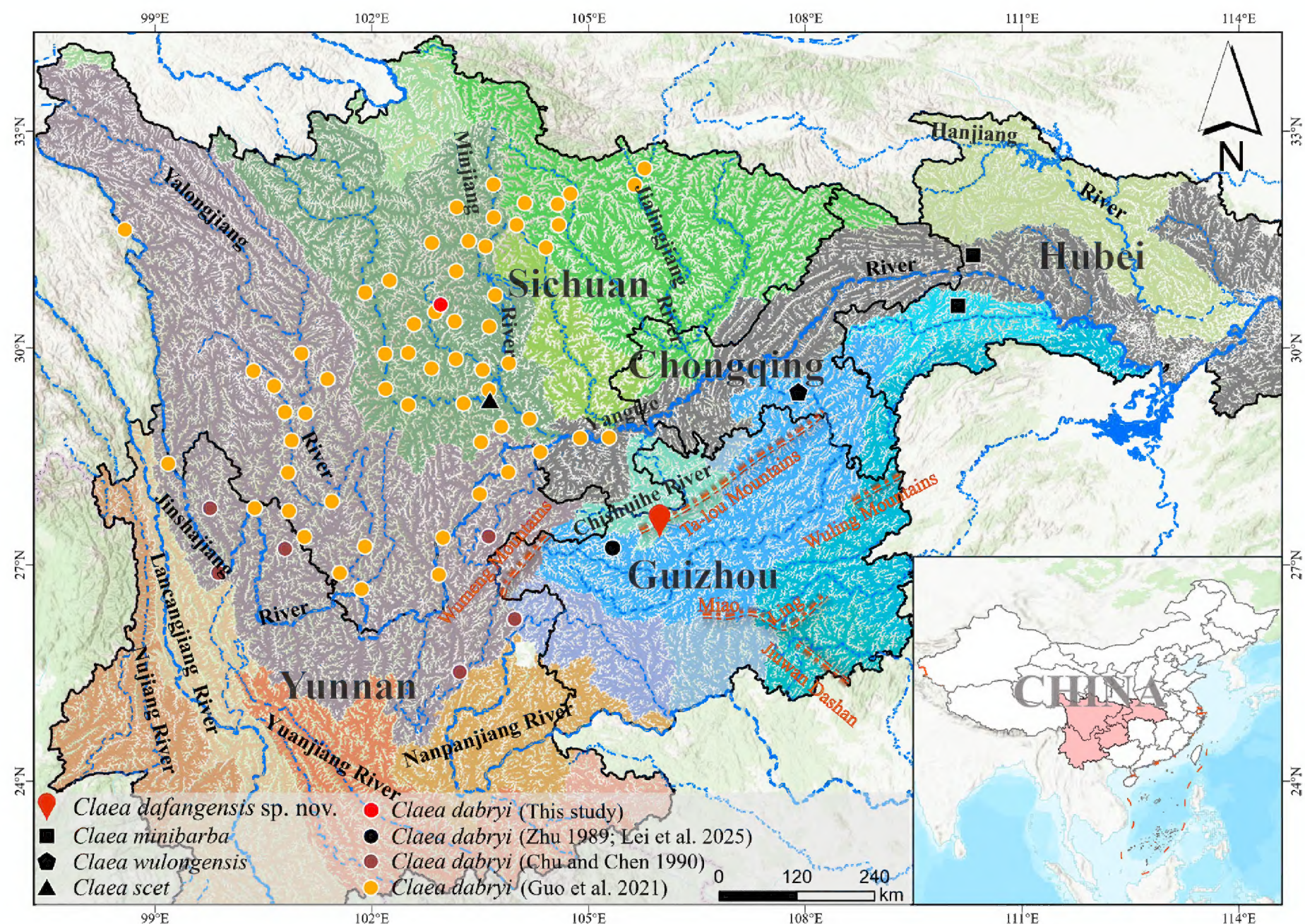


Figure 1. Distribution and sampling localities of the genus *Claea* and the new species in China.

Table 1. Localities, voucher information, and GenBank numbers for all samples used.

ID	Species	Localities (* type localities)	Voucher ID	Cyt b
1	<i>T. guizhouensis</i>	Lewang Town, Wangmo County, Guizhou, China	gznu09	KU987438
2	<i>T. yaluwang</i>	Maoying Town, Ziyun City, Guizhou, China*	GZNU20240118005	PQ117067
3	<i>T. longliensis</i>	/	SWU2016090300	MW582825
4	<i>T. sanduensis</i>	Zhonghe Town, Sandu County, Guizhou, China*	SWU20170613001	MW582822
5	<i>T. qini</i>	Houping Village, Wulong County, Chongqing, China*	/	ON528184
6	<i>T. xiangxiensis</i>	Feihu Cave, Hunan, China*	/	JN696407
7	<i>T. nandanensis</i>	Hechi City, Guangxi, China	SWU20151123046	MG697588
8	<i>T. tianeensis</i>	Bala Township, Tian ‘e County, Guangxi, China*	GZNU20230404003	OQ754124
9	<i>T. nasobarbatula</i>	Dongtang Township, Libo County, Guizhou, China*	GZNU20220313011	OQ241176
10	<i>T. macrocephala</i>	Lihu Town, Nandan County, Guangxi, China*	GZNU20230404002	OQ754123
11	<i>T. rosa</i>	/	F3911	MG697587
12	<i>T. qingzhenensis</i>	Qingzhen County, Guiyang City, Guizhou, China*	IHB 201911150004	MT700458
13	<i>T. wudangensis</i>	Wudang District, Guiyang City, Guizhou, China*	GZNU20230404010	OQ754131
14	<i>T. ziyunensis</i>	Maoying Town, Ziyun City, Guizhou, China*	GZNU20230529004	PQ117069
15	<i>T. erythraea</i>	Dalong Cave, Huayuan County, Hunan, China*	/	MG967615
16	<i>T. xuanweiensis</i>	Tangtang Town, Xuanwei City, Yunnan, China*	ASIZB223818	OL675196
17	<i>T. zhenfengensis</i>	Xinlongchang Town, Xingren City, Guizhou, China*	GZNU20220313007	OQ241177
18	<i>T. rongduensis</i>	Rongbei Town, Ceheng County, Guizhou, China*	GZNU20230110001	OQ754135
19	<i>T. anlongensis</i>	Xinglong Town, Anlong County, Guizhou, China*	GZNU20230112001	OQ754138
20	<i>T. baotianensis</i>	Baotian Town, Panzhou City, Guizhou, China*	GZNU20180421006	OQ241181
21	<i>T. panzhouensis</i>	Hongguo Town, Panzhou City, Guizhou, China*	GZNU20220513001	OQ754119
22	<i>T. cehengensis</i>	Rongbei Town, Ceheng County, Guizhou, China*	GZNU20230109001	OQ754132
23	<i>T. huapingensis</i>	Huaping Town, Leye County, Guangxi, China*	GZNU20230404004	OQ754125
24	<i>T. langpingensis</i>	Longping Township, Tianlin County, Guangxi*	GZNU20230404001	OQ754122
25	<i>T. qiubeiensis</i>	Nijiao Village, Qiubei County, Yunnan, China*	GZNU20230404006	OQ754127

ID	Species	Localities (* type localities)	Voucher ID	Cyt b
26	<i>T. wulongensis</i>	HuoLuTown, Wulong County, Chongqing City, China	GZNU20230404008	OQ754129
27	<i>T. wulongensis</i>	Wulong County, Chongqing, China*	/	MW582823
28	<i>T. nujiangensa</i>	Fugong County, Yunnan, China	IHB201315814	KT213598
29	<i>T. tibetana</i>	Mafamu lake, Xinjiang, China	NWIPB1106069	KT224364
30	<i>T. tenuis</i>	Niutou river, Qingshui County, Gansu, China	IHB0917490	KT224363
31	<i>T. wuweiensis</i>	Yongchang County, Gansu, China	IHB201307124	KT224365
32	<i>C. dafangensis</i> sp. nov.	Dafang county,Bijie City,Guizhou,China*	GZNU20241114008	PX703773
33	<i>C. dafangensis</i> sp. nov.	Dafang county,Bijie City,Guizhou,China*	GZNU20190804010	PX703774
34	<i>C. dabryi</i>	Qingyijiang river, Sichuan, China	GZNU20230728001	PX703772
35	<i>C. dabryi</i>	Dadu river, Sichuan, China	CWNU201407121	KX289615
36	<i>C. dabryi</i>	Minjiang river, Sichuan, China	CWNU201504001	KX394261
37	<i>C. dabryi</i>	Minjiang river, Sichuan, China	CWNU201504002	KX394262
38	<i>C. minibarba</i>	Hubei, China	IHB202204287749	OP750011
39	<i>C. minibarba</i>	Hubei, China	IHB202204287748	OP750012
40	<i>C. minibarba</i>	Hubei, China	IHB202204287747	OP750013
41	<i>C. minibarba</i>	Hubei, China	IHB2017097699	OP750014
42	<i>C. minibarba</i>	Hubei, China	IHB2017097698	OP750015
43	<i>C. scet</i>	Hulu Town, Leshan City, Sichuan, China*	IHB202305300003	PQ860813
44	<i>C. scet</i>	Hulu Town, Leshan City, Sichuan, China*	IHB202305300005	PQ860814
45	<i>B. barbatula</i>	/	/	KP715096
46	<i>B. labiata</i>	Xinyuan County, Xinjiang, China	IHB201306569	KT192057
47	<i>H. berezowskii</i>	Qujing City, Yunnan, China	FS-2014-Y03	NC040302

checked visually. Phylogenetic trees were constructed via both maximum likelihood (ML) and Bayesian inference (BI) methods. The ML analysis was conducted in IQ-TREE v. 2.0.4 (Nguyen et al. 2015) with 10,000 ultrafast bootstrap (UBP) replicates (Hoang et al. 2018), and it was performed until a correlation coefficient of at least 0.99 was reached. The BI analysis was performed in MrBayes v. 3.2.1 (Ronquist et al. 2012), and the best-fit model was obtained based on the Bayesian information criterion computed with PartitionFinder v. 2.1.1 (Lanfear et al. 2017).

The analysis suggested the best partition scheme for each codon position of Cyt *b*. SYM+I+G, GTR+I+G, and GTR+I+G were selected for the first, second, and third codon positions, respectively. Two independent runs were conducted in the BI analysis, each of which was performed for 10 million generations and sampled every 1000 generations. The first 25% of the samples were discarded as burn-in, resulting in a potential scale reduction factor of < 0.01. Nodes in the trees were considered well supported when Bayesian posterior probabilities (BPP) were ≥ 0.95 and the ML ultrafast bootstrap value (UBP) was ≥ 95%. Uncorrected *p*-distances (1000 replicates) based on Cyt *b* were estimated using MEGA v. 7.0 (Kumar et al. 2016).

Data availability statement

All data that support the findings of this study are available in the main text or Suppl. materials 1–3. Original sequence reads of genome data are available at the National Center for Biotechnology Information.

Results

Morphological analyses

Multivariate analysis revealed significant morphological differentiation between the new species and all congeners (Suppl. material 2), with particularly significant differences from *C. dabryi* (69% of characters significantly different, *p* = 0.00–0.03). The new species exhibits significant morphological differentiation from *C. wulongensis* in five key characteristics: standard length, predorsal length, preanal length, caudal peduncle length, and inter-orbital distance (Suppl. material 2).

PCA analysis extracted five principal component factors, which accounted for 78.54% of the total variation (Suppl. material 3). On the scatter plot of PC1 versus PC2, the new species was distinctly separated from *C. scet* and *C. minibarba* along the PC1 and PC2 axes (Fig. 2A). We also observed that the new species overlapped slightly, although it could be distinguished from *C. dabryi* and *C. wulongensis*. The canonical discriminant analysis (CDA) further confirmed these patterns, with the new species forming a distinct, non-overlapping cluster separate from the remaining four species in the discriminant space (Fig. 2B).

Phylogenetic reconstruction and genetic differences

The mitochondrial Cyt *b*-based phylogeny revealed that *Triplophysa* sensu lato comprises three major clades:

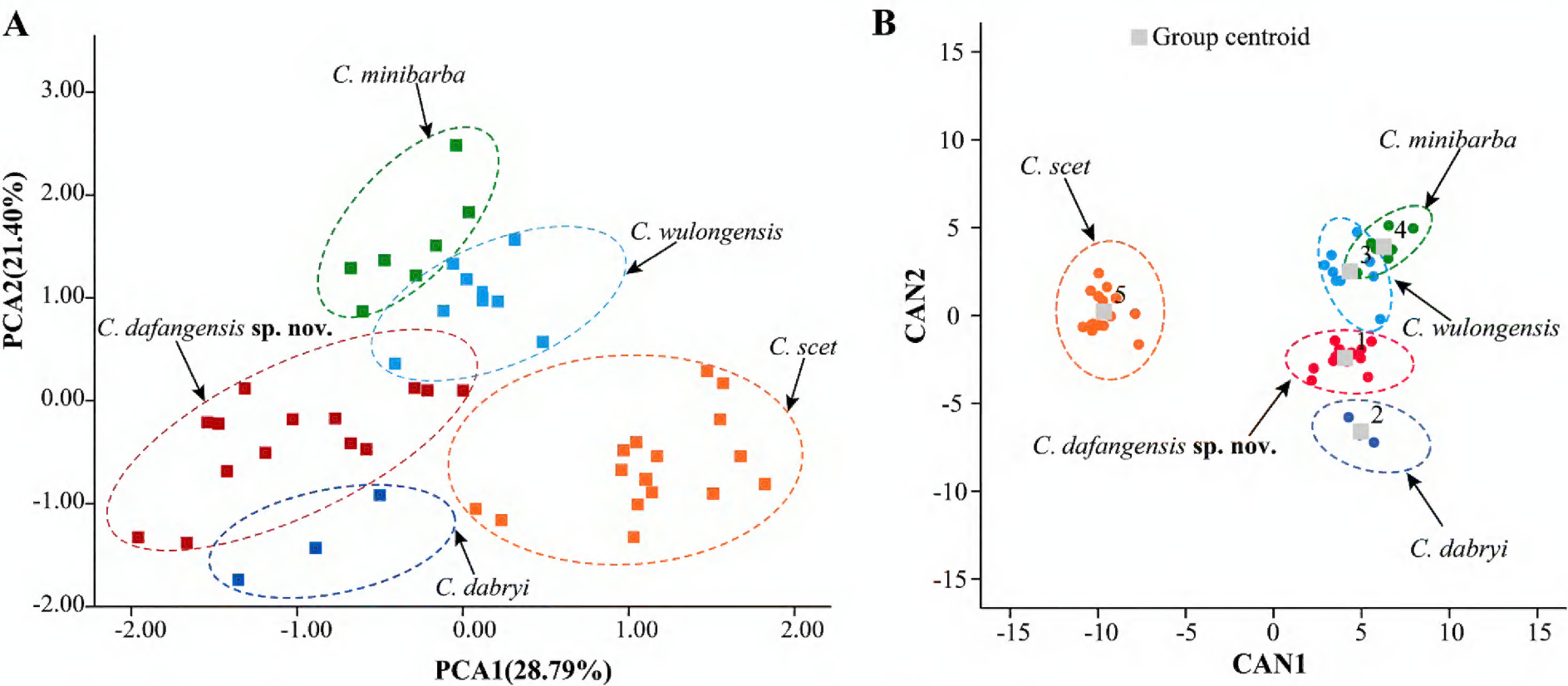


Figure 2. Plots of principal component analysis (A) and canonical discriminant analysis (B) scores of *C. dafangensis* sp. nov., *C. dabryi*, *C. wulongensis*, *C. minibarba*, and *C. scet* based on morphological characters.

Clade I and Clade III correspond to the epigeal and hypogean groups of *Triplophysa*, respectively, while Clade II represents the genus *Claea* (Fig. 3). Within the genus *Claea*, *C. scet* occupies the basal position. The population from Dafang, Guizhou, China, formed an independent lineage that was sister to *C. wulongensis* (BPP/UBP = 0.84/67). Notably, we observed that *C. dabryi* contained two clearly divergent lineages. The genetic distances between the new species and its congeners ranged from 2.6% (vs. *C. wulongensis*) to 5.7% (vs. *C. scet*) (Table 2).

Table 2. Uncorrected *p*-distances (%) among five species of the genus *Claea* based on mitochondrial Cyt *b*.

ID	Species	1	2	3	4	5
1	<i>Claea dafangensis</i> sp. nov.					
2	<i>Claea wulongensis</i>	2.6				
3	<i>Claea dabryi</i> (Dadu river, Qingyijiang river)	4.9	5.4			
4	<i>Claea dabryi</i> (Minjiang river)	3.7	4.5	2.8		
5	<i>Claea minibarba</i>	3.6	4.3	5.0	4.3	
6	<i>Claea scet</i>	5.7	6.0	6.7	6.2	5.8

Taxonomic account

***Claea dafangensis* Wang, Luo & Zhou, sp. nov.**
<https://zoobank.org/FAF5B19F-292F-4A3C-9C37-F4F4B04863AE>
Figs 4, 5A, Table 3

Chresonymy. *Schistura dabryi dabryi*: suburbs of Bijie City, Guizhou (Zhu 1989). Wujiang River in Bijie City, Guizhou (Lei et al. 2025). *Schistura dabryi*: upstream of the Wujiang River in Guizhou (Yang et al. 2022).

Type material. Holotype. GZNU20241204001 (Fig. 4), 88.08 mm total length (TL), 76.79 mm standard length (SL), collected by Jia-Jia Wang, Xin Xie, Yu-Ling Wang,

and Mei Liao on 4 December 2024, at Longtan Village, Yuchong Town, Dafang County, Guizhou Province, China (27.36265968°N, 105.98597243°E, 1376 m a.s.l.; Fig. 1).

Paratypes. Thirteen specimens from the same locality as the holotype: GZNU20190804001–006, GZNU20241204002–004, and GZNU20241114001–004, 49.36–80.15 mm SL, collected by Tao Luo, Xing-Liang Wang, Xin Xie, Yu-Ling Wang, Mei Liao, and Jia-Jia Wang in August 2019 and from November to December 2024.

Diagnosis. Comparative data between new species and all four known species within the genus *Claea* are provided in Table 3. *Claea dafangensis* sp. nov. can be distinguished from *C. scet* by the processus dentiformis prominent, covering lower jaw when mouth shut (vs. reduced, not covering lower jaw when mouth shut), body pigmentation present (vs. reduced), eyes normal, with diameter 10.9–21.0% of head length (HL) (vs. eyes reduced, 3.8–5.9% HL); from *C. minibarba* by tip of maxillary barbel reaching the posterior margin of eyes (vs. extending to the middle of eye), 8–9 branched pectoral-fin rays (vs. 10), and caudal-peduncle depth 6.1–8.7% SL (vs. 9.5–11.7%); from *C. wulongensis* by tip of maxillary barbel reaching the posterior margin of eye (vs. extending to anterior margin of eye), 16 branched caudal-fin rays (vs. 18), and interorbital width 23.6–39.0% HL (vs. 38.5–43.1%); from *C. dabryi* (Fig. 6) by outrostral barbel backward extending beyond the anterior nostrils (vs. reaching or beyond to anterior margin of eye), tip of maxillary barbel reaching the posterior margin of eye (vs. beyond the posterior margin of eye), and anal fin base length 4.0–5.5% SL (vs. 2.8–3.4%).

Description. Morphometric measurements of *Claea dafangensis* sp. nov. are summarized in Suppl. material 1.

Body elongated, anteriorly subcylindrical and posteriorly gradually compressed from dorsal fin to caudal-fin base, with maximum body depth at dorsal-fin origin, deepest body depth 8.8–15.5% of SL. Dorsal profile is

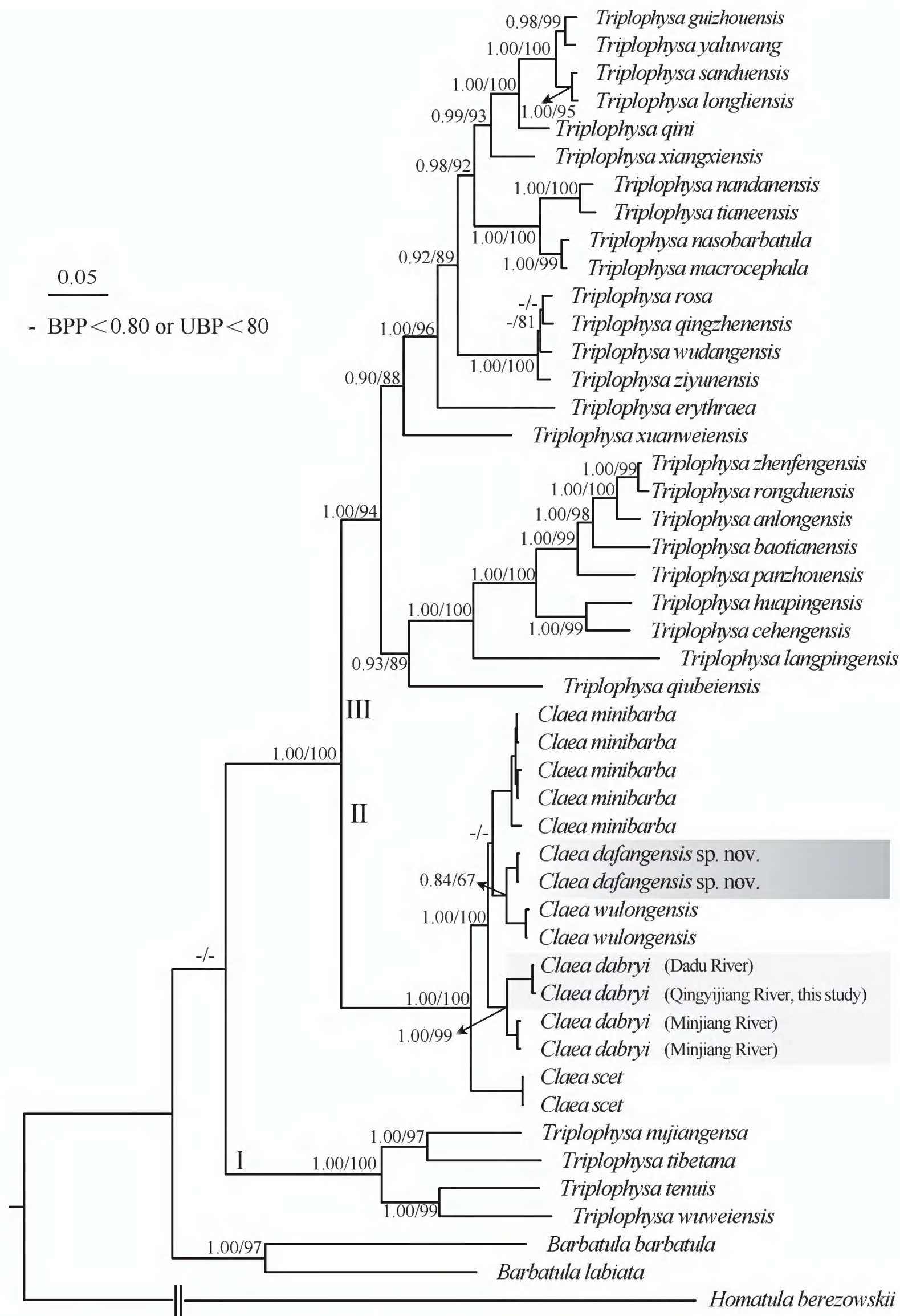


Figure 3. Phylogenetic tree reconstructed based on the mitochondrial *Cyt b*. In the phylogenetic trees, ultrafast bootstrap supports (UBP) from ML analyses and Bayesian posterior probabilities (BPP) from BI analyses are noted beside nodes. The scale bar represents 0.05 nucleotide substitutions per site.

not clearly elevated from snout to dorsal-fin insertion, and then straight from posterior portion of dorsal-fin origin to caudal-fin base. Head depressed, length 15.7–23.5% SL, Snout moderately blunt, length approximately 28.3–64.7% HL. Mouth inferior arched and curved,

mouth corner situated below anterior nostril, upper and lower lips smooth, with thin lips exhibiting shallow surface furrows, and lower lip with V-shaped median notch. Processus dentiformis prominent, covering lower jaw when mouth shut. Anterior and posterior nostrils closely

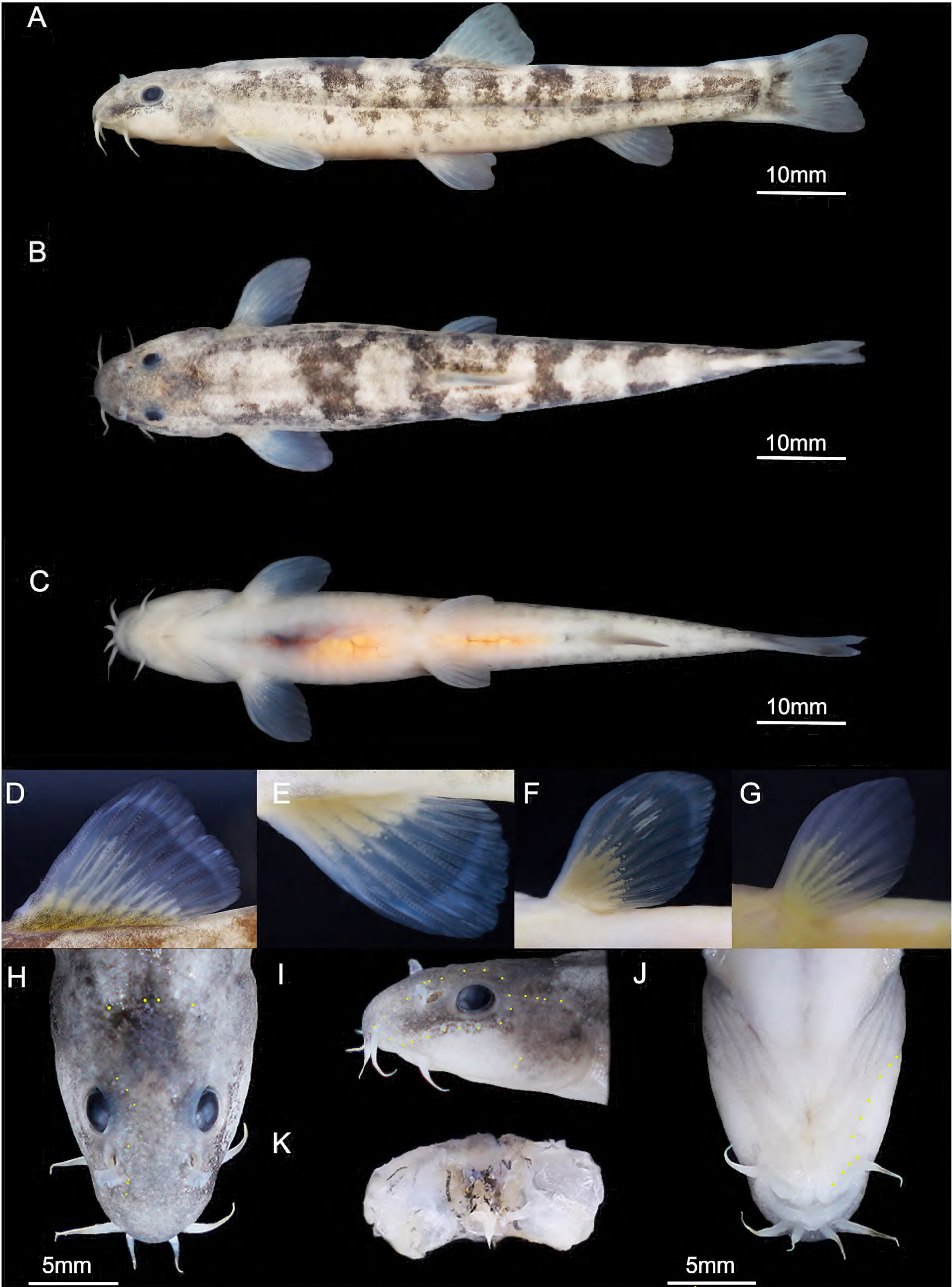


Figure 4. Holotype GZNU20241204001 (A–K) of *Claea dafangensis* sp. nov. in preservative. (A) Lateral view. (B) Dorsal view. (C) Ventral view. (D) Dorsal-fins view. (E) Anal-fins view. (F) Pectoral-fins view. (G) Pelvic-fins view. (H) Dorsal view of head. (I) Lateral view of head. (J) Ventral view of head. (K) Anterior chamber and posterior chamber. (Cephalic lateral line system highlighted as yellow dots)

Table 3. Diagnostic characters selected for the newly described species in this study and the four species of the genus *Claea*. Grey shading indicates clear differences in characteristics compared to those of *C. dafangensis* sp. nov.

Characters	<i>C. dafangensis</i> sp. nov.	<i>C. minibarba</i>	<i>C. dabryi</i>	<i>C. wulongensis</i>	<i>C. scet</i>
Eye	Normal	Normal	Normal	Normal	Reduced
Maxillary barbels (% HL)	18.6–43.8	21.5–29.6	23.1–32.7	21.8–35.9	22.4–37.4
Outer rostral barbels (% HL)	16.2–51.1	22.1–28.0	32.9–39.7	21.4–41.5	23.0–38.6
Body depth (% SL)	8.8–15.5	14.7–17.6	8.1–9.2	9.3–13.6	10.1–13.6
Pectoral-fin length (% SL)	13.8–18.3	15.0–17.6	13.6–14.8	15.6–18.4	15.6–22.0
Caudal peduncle depth (% SL)	6.1–8.7	9.5–11.7	6.5–6.9	7.6–9.4	5.5–8.5
Head depth (HL%)	40.0–64.9	55.5–59.4	43.2–48.9	45.3–54.2	40.4–56.1
Head width (HL%)	48.3–73.9	61.5–68.0	52.8–65.6	55.7–65.8	51.6–77.0
Anal-fin base length (% SL)	4.0–5.5	7.9–9.0	2.8–3.4	6.6–8.2	6.8–9.6
Pelvic-fin origin (% SL)	40.3–49.8	47.7–50.6	47.5–48.9	48.3–50.9	50.2–56.0
Interorbital width (% HL)	23.6–39.0	30.3–36.3	21.1–24.8	38.5–43.1	18.3–31.9
Pectoral-fin rays	i, 8–9	i, 10	i, 9	i, 8–9	i,10
Caudal-fin rays	16	18	16–17	18	16
Anal-fin rays	iii,5	i,5	ii,5	i,5–6	iii,5–6
Extension of outer rostral barbel to anterior margin of eye	No	Yes	Yes	No	No
Extension of maxillary barbel beyond posterior margin of eye	No	No	Yes	No	/
Extension of inner rostral barbel reaching the corner of the mouth	No	No	/	Yes	No

located; anterior nostril tube short, no distinct barbel-like at the tip of the anterior nostril, tip of posterior nostril backward extending not reaching to anterior margin of orbit. Three pairs of barbels, inner rostral barbel short, length 13.1–28.5% HL, backward extending not reaching the corner of the mouth; outrostral barbel short, length 16.2–51.1% HL, backward extending not reaching posterior margin of eyes, but beyond the anterior nostrils. Tip of Maxillary barbel reaching the posterior margin of eyes, length 18.6–43.8% HL. Eyes normal, with diameter 10.9–21.0% HL.

Dorsal-fin rays iii,8(n = 14), pectoral-fin rays i,8(n = 6)–9(n = 8), pelvic-fin rays i,6(n = 14), anal-fin rays iii-5(n = 14), and 16(n = 14) branched caudal-fin rays. Dorsal fin short, length 12.7–19.5% SL, distal margin truncated, origin posterior to pelvic-fin origin and situated slightly posterior to the midpoint between snout tip and caudal-fin base; first branched ray longest, shorter than head length; tip of the dorsal fin is located vertical but slightly in front of the anus. Pectoral fin short, length 13.8–18.3% SL, tip of pectoral fin backward extending almost to midpoint between origin of pectoral and pelvic-fin origins, not reaching to pelvic-fin origin. Pelvic fin short, length 10.1–14.7% SL, vertically aligned with third branched ray of dorsal fin, tips of pelvic fin not reaching the anus. Anal-fin length 11.3–14.9% SL, distal margin truncated, origin slightly separated form the anus, tips of anal fin not reaching caudal-fin base, Caudal fin forked, upper lobe slightly longer than lower lobe, caudal peduncle length 8.0–17.2 mm, caudal peduncle depth 3.0–6.7 mm, with weak adipose crests along both dorsal and ventral sides.

Body scaleless. Cephalic lateral-line system developed, with 7–9 supraorbital, 4–5 + 11–12 infraorbital canal pores, 3–4 supratemporal canal pores, with 9–10 preoperculo-mandibular canal pores. Lateral line complete and nearly straight, extending from behind extremity of gill opening along mid-lateral body to terminate middle caudal-fin base. Stomach U-shaped; intestine short, zigzag in shape posteriorto stomach. Two chambers of air bladder; anterior chamber enclosed in a dumbbell-shaped bony capsule and posterior chamber nearly completely degenerated (Fig. 4K).

Coloration. In freshly collected individuals (Fig. 5A), the body of living fish is yellowish, with irregular dark black patches on the head and body. After fixation in a 10% formalin solution, the body color was pale grey, and the dark-brown patches on the head and body were more prominent.

Secondary sex characteristics. No secondary sex characteristics were observed based on the present specimens of *Claea dafangensis* sp. nov.

Ecology and distribution. *Claea dafangensis* sp. nov. has only been found in a surface pool fed by a cave in Longtan Village, Yuchong Town, Dafang County, Guizhou Province, China, at an elevation of 1376 m. The pool where the new species was found is more than 21 m long and 20 m wide, with a slow flow of water, and it is located at the entrance of the cave. Inside the pool, tadpoles of *Oreolalax rhodostigmatus* were found. Beside the pool, rapeseed was being grown.

Etymology. The specific epithet “*dafangensis*” refers to the type locality of the new species, distributed in Dafang County. We propose the common English name “Dafang mountain loach” and the Chinese name “Dà Fāng Shān Qiū (大方山鳅).”

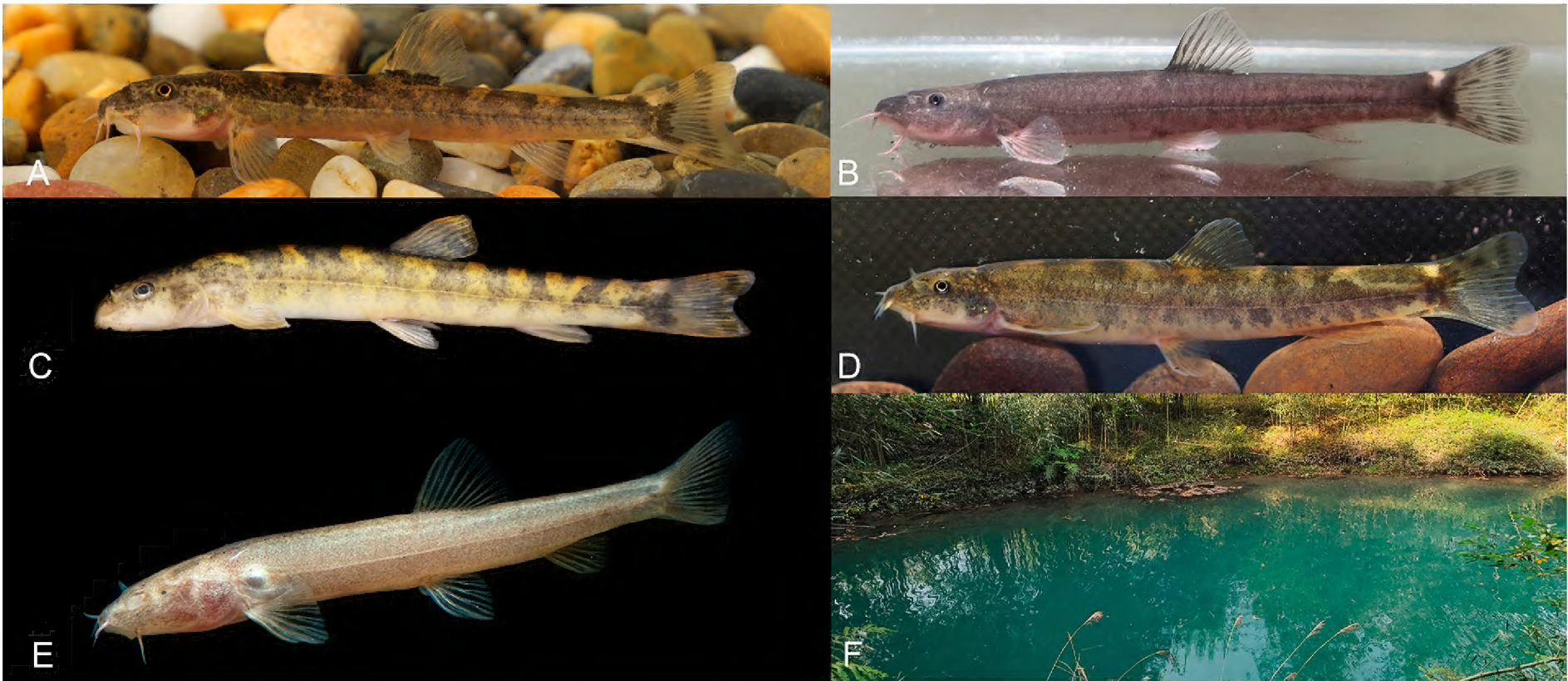


Figure 5. Lateral view of species in the genus *Claea* during life and the habitat of the new species. (A) *Claea dafangensis* sp. nov. (B) *C. dabryi*. (C) *C. wulongensis* (Chen et al. 2021). (D) *C. minibarba* (Zhang et al. 2024). (E) *C. scet* (Lei et al. 2025). (F) Habitat of *Claea dafangensis* sp. nov.



Figure 6. Morphological characteristics of *Claea dabryi* (GZNU20230723001) in 75% ethanol. (A) Lateral view. (B) Dorsal view. (C) Ventral view.

Discussion

The taxonomy of the genus *Triplophysa* has long posed significant challenges in systematics. Currently, *Triplophysa* is divided into two ecological groups: the epigean group (distributed across the Qinghai-Tibet Plateau and surrounding regions) and the hypogean group (restricted to karst caves in southwestern China). Although the genus *Claea* was proposed as a distinct genus in 2011 (Kottelat 2011), its phylogenetic position remained unclear until Yan (2017) first demonstrated its closer affinity to the hypogean group of the genus *Triplophysa*. However, this finding (published only in an unpublished master’s thesis) received little attention. Our results, consistent with Zhang et al. (2024), Lei et al. (2025), and Šlechtová et al. (2025), corroborate Yan’s (2017) phylogeny, revealing that *Claea* is nested within *Triplophysa* as a sister clade to the hypogean group (Fig. 3). The genus *Triplophysa* sensu lato comprises three distinct lineages: *Triplophysa* sensu stricto (epigean group), the genus *Claea*, and the hypogean group. Our phylogenetic analyses, combined with recent taxonomic advances (Kottelat 2012; Zhang et al. 2024; Lei et al. 2025; Šlechtová et al. 2025), indicate that *Triplophysa* requires revision. Given the validity of *Claea* as a genus, we propose elevating the hypogean group to generic status, supported by additional evidence, e.g., morphology, systematics, and its unique cave-dwelling ecology. However, this recommendation needs further comprehensive study.

In this study, we demonstrate, based on morphological and genetic evidence, that this population represents a previously unrecognized species, which we describe herein as *Claea dafangensis* sp. nov. Morphologically,

the new species is readily distinguishable from the four currently recognized congeners (see Diagnosis). Genetically, this population forms an independent phylogenetic lineage in the mitochondrial Cyt *b*-based phylogeny, with a minimum genetic distance of 2.6% from *C. wulongensis* (Table 2). Additionally, unpublished population genomic evidence from our study indicates no detectable gene flow between *Claea dafangensis* sp. nov. and other congeneric species, further supporting its recognition as a distinct and valid species.

The *Claea* populations in the upper Wujiang River, Guizhou, have undergone repeated taxonomic revisions, yet their phylogenetic placement remains unresolved. These populations were initially documented as *S. dabryi dabryi* in the suburbs of Bijie (Zhu, 1989) or as *S. dabryi* in the Chishui River and upper Wujiang River basins (Yang et al. 2022). Zhang et al. (2024) subsequently identified populations from the same basin as *C. minibarba*, while Lei et al. (2025) continued to refer to the upper Wujiang River populations as *C. dabryi*. Despite these revisions, the taxonomic status of upper Wujiang *C. dabryi* remains unclear due to insufficient integration of morphological and genetic evidence. Through detailed comparison with previously published morphological data, we found that these populations share similar morphological characteristics and exhibit overlapping morphometric values (Table 4). These results indicate that the populations previously identified as *S. dabryi dabryi*, *S. dabryi*, and *C. minibarba* in the Wujiang River basin in western Guizhou should be classified under the new species *Claea dafangensis* sp. nov., as described in this study.

Claea dabryi is a widely distributed species within the genus *Claea* (Fig. 1), recorded in the Minjiang, Jinshajiang,

Table 4. Morphological comparison between the new species and previously recorded *Claea* populations in the Wujiang River basin, western Guizhou.

	<i>C. dafangensis</i> sp. nov.	Zhu (1989)	Yang et al. (2022)
Dorsal-fin rays	iii, 8	iii–iv, 7–8	iii, 7–8
pectoral-fin rays	i, 8–9	i, 9–10	i, 8–10
pelvic-fin rays	i, 6	i, 6–7	i, 7
anal-fin rays	iii, 5	iii, 5	iii, 5
Caudal-fin rays	16	15–16	15–17
Body pigmentation	Present	Present	Present
Body scales	Absent	Absent	Absent
Eyes	Normal	Normal	Normal
Posterior chamber of air bladder	High degenerated	NA	Degenerated
Dorsal-fin origin	Posterior to pelvic-fin origin	Posterior to pelvic-fin origin	Posterior to pelvic-fin origin
Tip of pelvic fin	Not reaching the anus	Not reaching the anus	Not reaching the anus
Standard length/body depth	6.4–11.4	5.2–8.3	5.6–7.3
Standard length/head length	4.3–6.4	4.3–5.1	3.9–4.8
Standard length/caudal peduncle length	4.4–6.4	5.4–6.8	5.0–6.0
Head length/snout length	1.5–3.5	2.3–2.7	2.2–2.6
Head length/eye diameter	4.8–9.2	5.4–8.0	5.7–8.0
Head length/interorbital distance	2.6–4.2	3.1–4.0	3.1–4.0
Interorbital distance/eye diameter	1.2–2.4	1.2–2.4	NA
Caudal peduncle length/caudal peduncle depth	2.1–2.8	1.7–2.4	1.5–2.3

Jialingjiang, and the mainstream of the Yangtze River in Sichuan (Zhu 1989; Wu and Wu 1992; Ding 1994; Chen 1998; Kottelat 2012; Zhang et al. 2019; Guo et al. 2021); the Jinshajiang River basin in northern Yunnan (Zhu and Wang 1985; Zhu 1989; Wu and Wu 1992; Chen 1998; Zhang et al. 2019; Tian et al. 2022); the upper Wujiang River in western Guizhou (Zhu 1989; Yang et al. 2022); the lower Wujiang River in Chongqing (Tang et al. 2001); and the Qingjiang River in Hubei (Yang 1987; Tang et al. 2001). Among these, populations from Chongqing, Hubei, and Guizhou have recently been described as *C. wulongensis* (Chen et al. 2021), *C. minibarba* (Zhang et al. 2024), and the new species *Claea dafangensis* sp. nov. proposed in this study. The extensive geographical distribution and complex hydrological isolation suggest that this species likely represents a complex comprising multiple cryptic species. Our current evidence indicates that populations from different tributaries within the Minjiang River basin form independent evolutionary lineages (Fig. 3) and exhibit a certain degree of genetic differentiation (2.8%) (Table 2). This implies that populations from different river systems may harbor even greater genetic divergence. Therefore, we hypothesize that *C. dabryi*, similar to the widely distributed *Oreonectes platycephalus* (Yu et al. 2023; Lan et al. 2024; Luo et al. 2024; Zhong et al. 2024; Liao et al. 2025), constitutes a species complex encompassing multiple evolutionary lineages. Taxonomic revisions are urgently needed for populations across different basins, particularly in the Jinshajiang River basin of western Sichuan and northern Yunnan, to uncover their underestimated cryptic diversity for biodiversity conservation purposes.

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Supplementary material 1

Raw data of the type specimens of *C. dafangensis* sp. nov. and *C. dabryi*

Authors: Jia-Jia Wang, Tao Luo, Ming-Yuan Xiao, Xin Xie, Yu-Ling Wang, Huai-Qing Deng, Ning Xiao, Jiang Zhou

Data type: xlsx

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Link: <https://doi.org/10.3897/zse.102.172325.suppl1>

Supplementary material 2

Morphometric statistics and results of analysis of variance for *C. dafangensis* sp. nov. (Cda), *C. dabryi* (Cd), *C. wulongensis* (Cwl), *C. minibarba* (Cm), and *C. scet* (Cs)

Authors: Jia-Jia Wang, Tao Luo, Ming-Yuan Xiao, Xin Xie, Yu-Ling Wang, Huai-Qing Deng, Ning Xiao, Jiang Zhou

Data type: xlsx

Explanation note: All units are in mm. *P*-values are at the 95% significance level

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Supplementary material 3

Results and percentage of variance explained by principal component and discriminant function analyses

Authors: Jia-Jia Wang, Tao Luo, Ming-Yuan Xiao, Xin Xie, Yu-Ling Wang, Huai-Qing Deng, Ning Xiao, Jiang Zhou

Data type: xlsx

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